

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 23:11:45 : Search time 63.6 Seconds

(without alignments)
328.331 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987

Sequence: 1 MSLLNTKIKIFPKNQAFKNGE.....AKWKEGATLAPSLDLVKRI 188

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SID55/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID55/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID55/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID55/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID55/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID55/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID55/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID55/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID55/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID55/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID55/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID55/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID55/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID55/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID55/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID55/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID55/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID55/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID55/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID55/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID55/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID55/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970.5	98.3	187	22	AAU34488
2	963.5	97.6	187	22	AAU38121
3	963.5	95.3	189	22	AAU33822
4	644.5	65.3	189	22	AAU36816
5	644.5	65.3	189	22	AAU37159
6	644.5	65.3	189	22	AAU37549
7	626	63.4	186	20	AAW30615
8	605.5	61.3	187	22	AAU36183
9	563.5	57.1	187	22	AAU34998
10	546	55.3	145	22	AAU63080
11	497.5	50.4	1873	22	ABG14982

12	370.5	37.5	271	21	AAU33833
13	370.5	37.5	271	21	AAU34590
14	370.5	37.5	273	21	AAU33832
15	370.5	37.5	273	21	AAU34590
16	351.5	35.6	266	21	AAU38191
17	350.5	35.5	199	18	AAU23715
18	346.5	35.1	224	21	AAU65959
19	346.5	35.1	256	22	AAU68037
20	343.5	34.8	198	22	AAU68036
21	335.5	34.0	219	22	ABG36215
22	334	33.8	233	21	AAU33528
23	332	33.6	206	19	AAU70222
24	328.5	33.3	220	22	AAU61843
25	324.5	32.9	198	22	AAU68040
26	323	32.7	199	18	AAU69793
27	322.5	32.7	271	18	AAU12692
28	322.5	32.7	271	21	AAU13399
29	322.5	32.7	271	22	AAU62478
30	322.5	32.7	271	22	AAU68038
31	322.5	32.7	271	22	AAU68038
32	315	31.9	199	19	AAU70221
33	307.5	31.2	263	15	AAU63754
34	306.5	31.1	196	22	ABU62769
35	304.5	30.9	178	18	AAU69794
36	299.5	30.3	242	22	ABU57947
37	295	29.9	187	19	AAU62792
38	291.5	29.5	194	19	AAU62792
39	283	28.7	194	22	ABU58322
40	283	28.7	194	22	ABU58322
41	282.5	28.6	195	22	ABU57761
42	282.5	28.6	196	22	AAU38997
43	278.5	28.2	181	14	AAU39938
44	271	27.5	193	12	AAU14303
45	264.5	26.8	195	21	AAU13470

ALIGNMENTS

RESULT 1	AAU34488	standard; Protein; 187 AA.
XX	AAU34488	
XX	AAU34488	
XX	14-FEB-2002	(first entry)
DE	E. coli cellular proliferation protein #69.	
XX	Antisense; prokaryotic cellular proliferation protein;	
KW	antibiotic; antibacterial; drug design.	
KW	antibiotic; antibacterial; drug design.	
XX	Escherichia coli.	
OS	Escherichia coli.	
XX	WO200170955-A2.	
PN	27-SEP-2001.	
PD	27-SEP-2001.	
PF	21-MAR-2001; 2001WO-US09180.	
XX	21-MAR-2001; 2000US-191078P.	
PR	23-MAY-2000; 2000US-206848P.	
PR	26-MAY-2000; 2000US-207727P.	
PR	23-OCT-2000; 2000US-242578P.	
PR	27-NOV-2000; 2000US-253625P.	
PR	22-DEC-2000; 2000US-257931P.	
PR	16-FEB-2001; 2001US-269308P.	
XX	(ELIT-) ELITRA PHARM INC.	
PA	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	
PI	Yamamoto RT, Xu HH;	
XX		

DR WPI: 2001-611495/70.
DR N-PSDB: AAS52347.
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PS Example 3; Seq ID No 10081; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 187 AA:
Query Match 98.3%; Score 970.5; DB 22; Length 187;
Best Local Similarity 99.5%; Pred. No. 3e-104; Indels 1; Gaps 1;
Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MSLINTKIRPFKNQAFKNGEIEITFEKDEGRMSVFFFPADFTFVCCTELGDVADHYE 60
DB 1 mslintkirkpfnqafkngelieitfekdegrrwsv-ffypadftfvcptelgdvadyhe 59
QY 61 ELOKLGVDYAVSTDPHFKHKAHSSSETIARIKIAMIDPGALTRNPNRDEGLAD 120
DB 60 elqklgvdvavstcdhfhkwhsssetiakikyamjgdpqaltrndmredeglad 119
QY 121 RATEFVDPQGIIOALEVTAEGIGRDSADLLRKIKAAQYVAHPGEVCPAKMKEGATLAP 180
DB 120 ratfvdpggijqalevtaegigrdsadllrkikaagyaahpgevcpcakwkegatl 179
QY 181 SDDLVGKI 188
DB 180 sldlvgki 187
RESULT 2
AAU38121
ID AAU38121 standard; Protein; 187 AA.
XX
XX AAU38121;
XX
DT 14-FEB-2002 (first entry)
XX
DE *Salmonella typhi* cellular proliferation protein #12.
XX
XX Antisense; prokaryotic cellular proliferation protein;
XX antibiotic; antibacterial; drug design.
XX
OS *Salmonella typhi*.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US09180.
XX

PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELITR) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI: 2001-611495/70.
XX N-PSDB: AAS55980.
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PS Example 3; Seq ID No 13714; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 187 AA:
Query Match 97.6%; Score 963.5; DB 22; Length 187;
Best Local Similarity 97.9%; Pred. No. 2e-103; Indels 1; Gaps 1;
Matches 184; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
QY 1 MSLINTKIRPFKNQAFKNGEIEITFEKDEGRMSVFFFPADFTFVCCTELGDVADHYE 60
DB 1 mslintkirkpfnqafkngelieitfekdegrrwsv-ffypadftfvcptelgdvadyhe 59
QY 61 ELOKLGVDYAVSTDPHFKHKAHSSSETIARIKIAMIDPGALTRNPNRDEGLAD 120
DB 60 elqklgvdvavstcdhfhkwhsssetiakikyamjgdpqaltrndmredeglad 119
QY 121 RATEFVDPQGIIOALEVTAEGIGRDSADLLRKIKAAQYVAHPGEVCPAKMKEGATLAP 180
DB 120 ratfvdpggijqalevtaegigrdsadllrkikaagyaahpgevcpcakwkegatl 179
QY 181 SDDLVGKI 188
DB 180 sldlvgki 187
RESULT 3
AAU33822
ID AAU33822 standard; Protein; 189 AA.
XX
XX AAU33822;
XX
DT 14-FEB-2002 (first entry)
XX

DE Staphylococcus aureus cellular proliferation protein #98.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.
 OS Staphylococcus aureus.
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI: 2001-611495/70.
 DR N-PSDB: AAS51681.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 5318; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 189 AA:

Query Match 65.3%; Score 644.5; DB 22; Length 189;
 Best Local Similarity 64.2%; Pred. No. 2.1e-66;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

QY 1 MSLLTKIKPFKNQF--KNGFEITEKEDTGRMSVFFEPADFTFCPELDGVADH 58
 DB 1 msllnkelpftagaqfdpkqdkfkevtgdlkgswwv-vcltpadfstvcpeledlqng 59
 QY 59 YEELQKLGVDYAVSTDTHTFTKAWHSSSEETAKIKYAMIGDPTGALTFRNFMREDEGL 118
 DB 60 yeelqklgvnsvstetdthfthkawnhssdsatskilymngpsqcltrnfvldeatgl 119
 QY 119 ADRAFTVVDPOGIIAIEVTAEGIGROASDLRKIKAAQYVASHGCEVCPAWEKGEATL 178
 DB 120 aqrgftldpddvgvvaselnadqigrdsctlahkikaqyvrknpgevcapwakgeagaktl 179

QY 179 APSLDLVGKI 188
 DB 180 qpgldlvgki 189

RESULT 4
 AAU36816
 ID AAU36816 standard; Protein; 189 AA.
 XX
 AC AAU36816;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Staphylococcus aureus cellular proliferation protein #986.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI: 2001-611495/70.
 DR N-PSDB: AAS54675.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 12409; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 189 AA:

Query Match 65.3%; Score 644.5; DB 22; Length 189;
 Best Local Similarity 64.2%; Pred. No. 2.1e-66;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

OY		1	MSLINTKIKPEFNQAA--KNGEPIETTEOTEGRSMVFFEFFFPADTPFCPTELGVDYAH	58
		: : : : :		:
Dd		1	mslmlkellpftagdfdpkdkqfkevltgedllgyswsv-vcfipadfsivcoteledtgnq	59
OY		59	YEELOKLGADVAVSTDTHEFTTKAMHSSETTAKIYYAMIGDPTGALTRFDMWREDEGL	118
		: : : : :		:
Dd		60	yaelqklgyrvnvsystdctfnvkawhdhsdaaskiytmigdgscitlmfvvldaeatgl	119
OY		119	ADRATFVVDDPGCIIGAIEVTAGSIGHDASDLLRKRIKAQYVASHPGEVCPAKMKEEATL	178
		: : : : :		:
Dd		120	aqrgrffildpqdvvgqaseinadnglgdstactlkakkaaqyvvrknpegevpakweagatk	179
OY		179	APSIDLVGKI 188	
Dd		180	qpqldlvgki 189	
RESULT		5		
AAU37159				
D		AAU37159	standard; Protein; 189 AA.	
AC				
XX		AAU37159;		
DT		14-FEB-2002	(first entry)	
DE		Staphylococcus aureus cellular proliferation protein #1329.		
XX				
KW		Antisense; prokaryotic cellular proliferation protein;		
XX		antibiotic; antibacterial; drug design.		
OS		Staphylococcus aureus.		
XX				
PN		WO200170955-A2.		
PD		27-SEP-2001.		
XX				
PF		21-MAR-2001; 2001WO-US09180.		
PR		21-MAR-2000; 2000US-191078P.		
PR		23-MAY-2000; 2000US-206848P.		
PR		26-MAY-2000; 2000US-207727P.		
PR		23-OCT-2000; 2000US-242578P.		
PR		27-NOV-2000; 2000US-253625P.		
PR		22-DEC-2000; 2000US-257931P.		
XX		16-FEB-2001; 2001US-269308P.		
PA		(ELIT-) ELITRA PHARM INC.		
XX				
XX		Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;		
XX		Yamamoto RT, Xu HH;		
DR		MP1: 2001-611495/70.		
DR		N-P5DB; AAS55018.		
XX				
PJ		New polynucleotides for the identification and development of		
XX		antibiotics, comprise sequences of antisense nucleic acids -		
PS		Example 3; Seq ID No 12752; 511pp; English.		
CC		The invention relates to antisense inhibitors of genes essential to		
CC		prokaryotic cellular proliferation, their use in identifying the		
CC		genes, their use in the discovery of novel antibiotics, the essential		
CC		themselves and the encoded proteins. The prokaryotes used are		
CC		Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella		
CC		pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The		
CC		invention is also useful for the identification of potential new targets		
CC		for antibiotic development. The antisense nucleic acids can also be used		
CC		to identify proteins used in proliferation, to express these proteins,		
CC		and to obtain antibodies capable of binding to the expressed proteins.		
CC		The proteins can be used to screen compounds in rational drug discovery		
CC		programmes. The antisense nucleic acid sequence is also useful to screen		
CC		for homologous nucleic acids which are required for cell proliferation in		

CC	a wide variety of organisms. The present sequence represents an
CC	essential prokaryotic cellular proliferation protein.
CC	Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic
CC	format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
SQ	Sequence 189 AA:
Query Match	65.3%; Score 644.5; DB 22; Length 189;
Best Local Similarity	64.2%; Pred No. 2.1e-66;
Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2.	
OY	1 MSLLNTKIKPFKNQAF-KNGEFILTEKDTGSRVSFFFYPADFTVCPTGLDVA
DB	1 mlllnkellpfatgaqdkpqdkgfkevtgdlkgsww-vcfypadtsfcpcleedlgnq 59
OY	59 YEELOKLGVAVSTIDTHFKAMHSSETTAKIKYAMIGPFGALTRNFDNRDECL 118
DB	60 yeeqlqlygvsvstldtfvhwkwhdsdaiskilytmigpsqtltntfvldeatgl 119
OY	119 ABRATFVVDPOGIIAEVTAGIGDGASDLRKTKAAQYVASHPGEVCPARKKEEATL 178
DB	120 aqrftllipddvgaseinadqigrdasclahklkaagvytknpgevcparkeeagactl 179
OY	179 APSLDLVGKI 188
DB	180 qp9ldlvgtkl 189
RESULT 6	
AAU37549	
ID	AAU37549 standard; Protein; 189 AA.
XX	AAU37549;
AC	14-FEB-2002 (first entry)
DT	
XX	
XX	Staphylococcus aureus cellular proliferation protein #1719.
DE	
XX	
KW	Antisense; prokaryotic cellular proliferation protein;
KW	antibiotic; antibacterial; drug design.
XX	
OS	Staphylococcus aureus.
XX	
PN	WO200170955-A2.
XX	
PD	27-SEP-2001.
XX	
PX	
PF	21-MAR-2001; 2001WO-US09180.
XX	
PR	21-MAR-2000; 2000US-191078P.
PR	23-MAY-2000; 2000US-206848P.
PR	26-MAY-2000; 2000US-207727P.
PR	23-OCT-2000; 2000US-242578P.
PR	27-NOV-2000; 2000US-253625P.
PR	22-DEC-2000; 2000US-257931P.
PR	16-FEB-2001; 2001US-269308P.
PA	(ELIT-) ELITRA PHARM INC.
PI	
PI	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr CJ,
PI	Yamamoto RT, Xu HH;
XX	
XX	WPI; 2001-611495/70.
DR	N-PSDB; AAS55408.
PT	New polynucleotides for the identification and development of
PT	antibiotics, comprise sequences of antifission nucleic acids -
XX	
XX	Example 3; Seq ID NO 13142; 511pp; English.
XX	

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 139 AA;

Query Match 65.3%; Score 644.5; DB 22; Length 189;
Best Local Similarity 64.2%; Pred. No. 2.1e-66;
Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

QY 1 MSLINTKIKPKKNOAF-KNGEPIETEKDEGRMSVFFFFYPADFTVCPTLEGVADH 58
DB 1 mslintkikpftagaftbkqdkfkevtdlkgswsv-vctfpadfsivcpteledlqng 59
QY 59 YEELOKLSDVDYAVSTDPHFTKAMHSSSETIAKIKYAMIGDPGALTRNFDNMRDEGL 118
DB 60 yeeloklsgvavsvstphftkhamhsssetiaikykamigdpqaltrnfdnmredgl 119
QY 119 ADRAFFVDPGIIQAEIVTAEGIGRSDLLRRIKAQYVASHPGECVPAKWKEGEATL 178
DB 120 adrgtffldpdyvqaseinadgigrdastlahkkaayrvkrngpvcvpaekweegaktl 179
QY 179 APSLDVWGI 188
DB 180 qpsldlvwgi 189

RESULT 7

AAW30615 standard; Protein: 186 AA.

AAW30615:
31-MAR-1999 (first entry)
Streptococcus mutans alkyl hydroperoxide reductase.
Streptococcus mutans; alkyl hydroperoxide reductase; NADH oxidase;
Nox-1; water; hydrogen peroxide.
Streptococcus mutans.

XX Key Location/Qualifiers
FH Misc-difference 156 /note= "encoded by TCT"
FT Misc-difference 181 /note= "encoded by GTA"
XX JP11004690-A.
XX 12-JAN-1999.
XX 17-JUN-1997; 97JP-0160319.
XX 17-JUN-1997; 97JP-0160319.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI: 1999-135784/12.
DR N-PSDB: AAX00499.
XX
PT Alkyl hydroperoxide reductase gene - converts hydrogen peroxide
PT produced by NADH oxidase Nox-1 to water
XX
PS Claim 1; Page 4-5; 7pp; Japanese.
CC The present sequence represents alkyl hydroperoxide reductase from
CC Streptococcus mutans. The alkyl hydroperoxide reductase gene can
CC convert hydrogen peroxide formed by Nox-1 to water.
XX
SO Sequence 186 AA;

Query Match 63.4%; Score 626; DB 20; Length 186;
Best Local Similarity 60.6%; Pred. No. 2.9e-64;
Matches 114; Conservative 29; Mismatches 43; Indels 2; Gaps 2;

QY 1 MSLINTKIKPKKNOAFKNGEPIETEKDEGRMSVFFFFYPADFTVCPTLEGVADH 60
DB 1 mslvgkemvetsagayhbgelvtvnedvkgkwav-fctfpadfsivcptelgldqeyga 59
QY 61 ELQKIGVAVVSTDPHFTKAMHSSSETIAKIKYAMIGDPGALTRNFDNMRDEGLAD 120
DB 60 elqsigvavsvstphftkhamhsssetiaikykamigdpqaltrnfdnmredglad 118
QY 121 RATEVVPDGIQAEIVTAEGIGRSDLLRRIKAQYVASHPGECVPAKWKEGEATLAP 180
DB 119 rgtffvdpdgiilqgmvnadvgrdstlckvtraaqylrqhpgvcpakwkgeatlkp 178
QY 181 SLDLVWGI 188
DB 179 sldlvwgi 186

RESULT 8

AAU36183 standard; Protein: 187 AA.

AAU36183:
14-FEB-2002 (first entry)
Pseudomonas aeruginosa cellular proliferation protein #173.
Antisense: prokaryotic cellular proliferation protein;
antibiotic; antibacterial; drug design.
Pseudomonas aeruginosa.

XX WO200170955-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US09180.
XX 21-MAR-2000; 2000US-191078P.
XX 23-MAY-2000; 2000US-206848P.
XX 26-MAY-2000; 2000US-207727P.
XX 23-OCT-2000; 2000US-242578P.
XX 27-NOV-2000; 2000US-253625P.
XX 22-DEC-2000; 2000US-257931P.
XX 16-FEB-2001; 2001US-269308P.
XX (ELIT-) ELITRA PHARM INC.
XX Haselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX Yamamoto RT, Xu HH;
XX WPI: 2001-611495/70.

DR N-PSDB; AAS54042.

XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX
PS Example 3; Seq ID No 11776; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 187 AA:

Query Match 61.3%; Score 605.5; DB 22; Length 187;
Best Local Similarity 58.5%; Pred. No. 6,9e-62;
Matches 110; Conservative 32; Mismatches 45; Indels 1; Gaps 1;

QY 1 MSINIKIRPFKNQAKNEFIETKDEGRMSVFFFPADFTVCTELGDVADHYE 60
DB 1 msinikirpfknqaknefietskdegrmsvfffpadftvctelgdvadye 59
QY 61 ELQKLGVDYAVSTDTFHFKAMHSSSETIAKIKYAMIDPTGALTRNPDNMRDEGLAD 120
DB 60 elqklgvdvavstdtfhfkamhsssetiakikyamidptgaltrnpsdneeglal 119
QY 121 RATEVVDPOGIIQALIEVTAGIGRDSDLIRKIKAAQYVASHPEVCAPKWKEGEATLAP 180
DB 120 rgefivnpgevlktveihnselardgetvrkkaeqyaahpgevcapkwkegektlap 179
QY 181 SLDLVGKI 188
DB 180 sldlvgki 187

RESULT 9
AAU34998 standard; Protein; 187 AA.

XX AAU34998;
XX
DT 14-FEB-2002 (first entry)
XX
DE Enterococcus faecalis cellular proliferation protein #285.
XX
KW Antisense; prokaryotic cellular proliferation protein;
XX antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
PD
XX 27-SEP-2001.
XX
PF 21-MAR-2001; 2001MO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS52857.

PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX
PS Example 3; Seq ID No 10591; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 187 AA:

Query Match 57.1%; Score 563.5; DB 22; Length 187;
Best Local Similarity 54.3%; Pred. No. 5,2e-57;
Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSINIKIRPFKNQAKNEFIETKDEGRMSVFFFPADFTVCTELGDVADHYE 60
DB 1 msinikirpfknqaknefietskdegrmsvfffpadftvctelgdvadye 59
QY 61 ELQKLGVDYAVSTDTFHFKAMHSSSETIAKIKYAMIDPTGALTRNPDNMRDEGLAD 120
DB 60 hlgelncevysvedshykhkewadatelgkikymldpngqlarffgviddeasgmay 119
QY 121 RATEVVDPOGIIQALIEVTAGIGRDSDLIRKIKAAQYVASHPEVCAPKWKEGEATLAP 180
DB 120 rasfivspgelksyeindmgigraeeelvrkkaeqyaahpgevcapkwpggeetlap 179
QY 181 SLDLVGKI 188
DB 180 sldlvgki 187

RESULT 10
AAU63080 standard; Protein; 145 AA.

XX AAU63080;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #23976.

Db 850 thftkwhssetlaklyamigqptgltrnfndmredegladratfvwpggllqai 909
Oy 136 EVTAEIGRDSDLRKIKAAQYVASHP 163
|||||
Db 910 evtlaegigrdasdlrkikaaqyashp 937

RESULT 12
AAG23833
ID AAG23833 standard; Protein: 271 AA.
XX
AC AAG23833;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27285.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
SS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 23-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
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PR 01-JUN-1999; 99US-0137222.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.

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PR 23-JUN-1999; 99US-0140354.
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PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142134.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 12-JUL-1999; 99US-0142927.
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PR 21-JUL-1999; 99US-0144814.
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PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145089.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.


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PR 13-AUG-1999; 99US-0148565.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.5%; Score 370.5; DB 21; Length 271;
Best Local Similarity 38.3%; Pred. No. 2,2e-34;
Matches 70; Conservative 39; Mismatches 71; Indels 3; Gaps 1;
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Oy 1 MSLINTKIKPFKNQAFKNEFIETEKDEGRMSVFFFPYPADFTFVCTELGDVADHRE 60
Db 77 IPIVGNKAPDIEAEVfGdEIKVlseyIqKkYvllfIfyIdftfcpteltatsdrye 136
Oy 61 ELQKGVVYAVSTDTDFHTKAM--HSSSEETIAKIKYAMIDPFGALTRFNDNKRDEG 117
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DB 137 efekIntevlysvsdlawqtdrksqglgdlngplyvdsdtkslskstfgvllpdaq 196
Oy 118 LADRAATFVVDPOGIIQALIEVTAEGIGRDASDLLKRIKAQYVASHPEVCPAKKKEGERT 177
Db 197 IalrgIffIdkeqyIghstInlIgrsvdetmrtIqelqYvqenpdevcpgwKpgeks 256
Oy 178 LAP 180
Db 257 mKp 259

RESULT 13
AAG45901
ID AAG45901 standard; Protein; 271 AA.
AC AAG45901;
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SPO ID NO: 57685.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
XX PF 25-FEB-1999; 99US-0121825.
XX XX 05-MAR-1999; 99US-0123180.
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PR 25-MAR-1999; 99US-0126264.
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PR 18-MAY-1999; 99US-0134768.
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PR 01-JUN-1999; 99US-0137222.
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PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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 PR 30-JUN-1999; 99US-0140991.
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 PR 02-JUL-1999; 99US-0142154.
 PR 06-JUL-1999; 99US-0142055.
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Listing first 45 summaries

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; Patent No. 5744593

GENERAL INFORMATION:

APPLICANT: Klimowski, Laura

TITLE OF INVENTION: PARASITIC HELMINTH LARVAL THIOI SPECIFIC

TITLE OF INVENTION: ANTIOXIDANT PROTEINS, NUCLEIC ACID MOLECULES, AND USES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: CO

COUNTRY: U.S.A.

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602, 262

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-45

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700

TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-602-262-2

Query Match 35.4%; Score 349.5; DB 1; Length 199;
Best Local Similarity 39.4%; Pred. No. 4.4e-34;
Matches 69; Conservative 38; Mismatches 63; Indels 5; Gaps 3;

OY 11 FENQAFKGEFLEIEKTEGRMSVFFFFYPADFFVPCTELGDVADVAHEELQKGVY 70
Db 17 FETAVVNGDFEKEISLCOFKRY-VVLEFFYPIDFFVCPTEIIAFSDRIAEKKIDVAVM 75

COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 2; Length 257;
 Best Local Similarity 38.5%; Pred. No. 1.8e-32;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFLIEITEKDEGRMSVFEFFYPADFTFVCPTELGVDVADHYEELQKLGVDY 70
 DB 73 FKGTAVVNGEFLSLDDEKRGKYL-LFFYPPLDFTFVCPTEIIVASDKANFEHVDNCEVY 131
 QY 71 AVSTDHFTFKAMHSSSE---IAKIKYAMIGDPTGALTRFNDNMREDEGLADRATFVVD 127
 DB 132 AVSVSHSHFLAMINPRKNGGIGHNITLLSDITKQISRDYGVLESAGIALRGILFIID 191
 QY 128 PGQITQALIEVTAEGIGRDAADLLRRIKAKQVYASHGECVCPAKMKEGEATLAPS 181
 DB 192 PNGVVKHLVNDLPGRSVEETRLRYKAFQVETH-GEVCPANWIPESPTIKPS 244

RESULT 7
 US-08-467-265-16
 Sequence 16, Application US/08467265
 Patent No. 6255079
 GENERAL INFORMATION:
 APPLICANT: NI, Jian
 Yu, Guo-Liang
 Gentz, Reiner
 Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-Jun-1995
 CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 4; Length 257;
 Best Local Similarity 38.5%; Pred. No. 1.8e-32;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFLIEITEKDEGRMSVFEFFYPADFTFVCPTELGVDVADHYEELQKLGVDY 70
 DB 73 FKGTAVVNGEFLSLDDEKRGKYL-LFFYPPLDFTFVCPTEIIVASDKANFEHVDNCEVY 131
 QY 71 AVSTDHFTFKAMHSSSE---IAKIKYAMIGDPTGALTRFNDNMREDEGLADRATFVVD 127
 DB 132 AVSVSHSHFLAMINPRKNGGIGHNITLLSDITKQISRDYGVLESAGIALRGILFIID 191
 QY 128 PGQITQALIEVTAEGIGRDAADLLRRIKAKQVYASHGECVCPAKMKEGEATLAPS 181
 DB 192 PNGVVKHLVNDLPGRSVEETRLRYKAFQVETH-GEVCPANWIPESPTIKPS 244

RESULT 8
 US-09-407-891-16
 Sequence 16, Application US/09407891
 Patent No. 6294164
 GENERAL INFORMATION:
 APPLICANT: NI, Jian
 Yu, Guo-Liang
 Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-407-891-16

Query Match 34.2%; Score 337.5; DB 4; Length 257;
Best Local Similarity 38.5%; Pred. No. 1.8e-32;
Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

OY 11 FKNQKNGEIEITEKDEGRMSVFFFPYADFTFCVTELGADVADHEELQKLGVDY 70
DB 73 FKGTVANGEFKEKELSDPKKLYL-LFFYPLDFTFCVTELVASDKANEFHDVANCEV 131
OY 71 AVSTDTHFTKAMHSSSET--IAKIKYAMIGDPTGALTRNFMNREDEGLADRAFTVVD 127
b 132 AVSDSHFSLAMIMPRKNGSLGHMNTLLSDITKQISROYGLLESAGIALRGFLIID 191
OY 128 PGGITQALEVTAEIGGRDASDLRKIKAAQYVASHPEVCAPKMKEGEATLAPS 181
DB 192 PNGVVKHLSVNDLPVGRSVEETLRILVKAQFVETH-GEVCPANMTPEPTIKPS 244

RESULT 9

US-08-467-265-17
Sequence 17, Application US/08467265
Patent No. 5985612

GENERAL INFORMATION:

APPLICANT: NI, Jian
APPLICANT: Yu, Guo-liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-265-17

Query Match 33.3%; Score 329; DB 2; Length 199;

Best Local Similarity 35.6%; Pred. No. 1.3e-31;
Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

OY 1 MSLINTKI-----KPRKNOA-FKNGEIEITEKDEGRMSVFFFPYADFTFCVTELG 55
DB 1 MSSGNKIGYPAVPANFKAIVMPDGOFKDISLSEYKGY-VVEFFYPLDFTFCVTEIIAF 59
OY 56 ADHEELQKLGVDYAVSDTHFTKAMHSSSET--IAKIKYAMIGDPTGALTRNFDNM 112
DB 60 SDRADPEFKLNCQVIGASVDSHFCHLAWINTKKGGLGPMNPLISDPKRTIADYGL 119
OY 113 REDEGLADRAFTVVDQGITQALEVTAEIGGRDASDLRKIKAAQYVASHPEVCAPKMK 172
DB 120 KADEGISFRGLFIIDKILROITINDLPVGRSVDEIRLVQAQFTDKH-GEVCPAGMK 178
OY 173 EGEATLAPSLD 183
DB 179 PGSDTIKPDVN 189

RESULT 10

US-08-467-265-17
Sequence 17, Application US/08467265
Patent No. 6255079

GENERAL INFORMATION:

APPLICANT: NI, Jian
APPLICANT: Yu, Guo-liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-467-265-17

Query Match 33.3%; Score 329; DB 4; Length 199;
Best Local Similarity 35.6%; Pred. No. 1.3e-31;
Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

OY 1 MSLINTKI-----KPRKNOA-FKNGEIEITEKDEGRMSVFFFPYADFTFCVTELG 55
DB 1 MSSGNKIGYPAVPANFKAIVMPDGOFKDISLSEYKGY-VVEFFYPLDFTFCVTEIIAF 59

; Sequence 14, Application US/08467265
; Patent No. 5965612
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: YU, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,265
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-265-14

Query Match 32.7%; Score 323; DB 2; Length 199;
Best Local Similarity: 36.8%; Pred. No. 6.7e-31;
Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;
QY 1 MSLLNTKI---KPFKNOA-FKNGFEIETTEKDEGRWSVFFFPADFTFVCPTIELGDV 55
DB 1 MSSGNKIKGHPANFKATAMPDGQFKDISLSDYKGY-VVFFFYPLDFTFVCPTIELIAF 59
QY 56 ADHYEELQKLVYAVVSTDTHTFTKAMHSSSET---IAKIKYAMIGDPTGALTRFNDNM 112
DB 60 SDRAEFFKRLNCQVIGASVDSHCHLAWNTPKKGGGLGPMNIPLVSDPKRTIAODYGYL 119
QY 113 REDEGLADRTFVVDQGIIOALEVTAEGIGRASDLRLKRIKAOYVASHPGVCPAKWK 172
DB 120 KADEGISFRLIIDDKILRQITVNDPPCCRSVDETLRLVQAFOTDKH-GEVCPAGWK 178
QY 173 EGEATLAPSL 182
DB 179 PGSDTIKPDV 188

RESULT 14
US-08-467-265-14
; Sequence 14, Application US/08467265
; Patent No. 6255079
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: YU, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,265
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-467-265-14

Query Match 32.7%; Score 323; DB 4; Length 199;
Best Local Similarity 36.8%; Pred. No. 6.7e-31;
Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;
QY 1 MSLLNTKI---KPFKNOA-FKNGFEIETTEKDEGRWSVFFFPADFTFVCPTIELGDV 55
DB 1 MSSGNKIKGHPANFKATAMPDGQFKDISLSDYKGY-VVFFFYPLDFTFVCPTIELIAF 59
QY 56 ADHYEELQKLVYAVVSTDTHTFTKAMHSSSET---IAKIKYAMIGDPTGALTRFNDNM 112
DB 60 SDRAEFFKRLNCQVIGASVDSHCHLAWNTPKKGGGLGPMNIPLVSDPKRTIAODYGYL 119
QY 113 REDEGLADRTFVVDQGIIOALEVTAEGIGRASDLRLKRIKAOYVASHPGVCPAKWK 172
DB 120 KADEGISFRLIIDDKILRQITVNDPPCCRSVDETLRLVQAFOTDKH-GEVCPAGWK 178
QY 173 EGEATLAPSL 182
DB 179 PGSDTIKPDV 188

RESULT 15
US-09-407-891-14
; Sequence 14, Application US/09407891
; Patent No. 6294164
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: YU, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road

CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Feltaro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-407-891-14

Query Match 32.7%; Score 323; DB 4; Length 199;
Best Local Similarity 36.8%; Pred. No. 6.7e-31;
Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;

QY 1 MSLINTKI---KPKKQA-FKNGEPIETKDEGRMSVFEFFYPADFTFVCPTELGDV 55
DB 1 MSGNKKIGHAPNFKATVMPDGGFKDISLDYKGY-VFFFFPLDFTFVCPTEIIAF 59
QY 56 ADHYEELQKLGVDYAVSTDTHTKRAHSSSET---IAKIKYAMIGDPTGALTNRFDNM 112
DB 60 SDRAEFFKLNCOVIGASVDSHFCFLAWNTPEKOGGLGPMNIPLVSDPKRTIAQDYGL 119
QY 113 REDEGLADRAFTVDPGIIQAEVTAEGIGRDSPLRKIKAAQYVASHPGVCPAKMK 172
DB 120 KADEGISFGLFTIIDKGLRQITVNDPPCRSVDETLRLVQAFQFTDKH-GEVCPAGMK 178
QY 173 EGEATLAPSL 182
DB 179 PGSDTIKPDV 188

Search completed: May 19, 2002, 01:15:02
Job time: 7152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 19, 2002, 00:29:30 ; Search time 51.62 Seconds

(without alignments)
349.957 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987

Sequence: 1 MSLLNTRKIPFKNQAFKNGE.....AKWKEGPAFLAPSLDVGKI 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970.5	98.3	187	2	JN0289
2	970.5	98.3	187	2	D90709
3	970.5	98.3	187	2	H85559
4	963.5	97.6	187	2	H80577
5	742.5	75.2	187	2	D87610
6	714	72.3	206	2	G82668
7	677.5	68.6	187	2	F69583
8	644.5	65.3	189	2	F69804
9	624.5	63.3	168	2	PS0179
10	622.5	63.1	184	1	A35441
11	612.5	62.1	179	2	S52934
12	605.5	61.3	187	2	C83627
13	603.5	61.1	187	2	A86667
14	488.5	49.5	188	2	D71314
15	455.5	46.1	211	2	G70343
16	365	37.0	242	2	S49173
17	362	36.7	210	2	T06318
18	361	36.6	198	2	A57716
19	354	35.9	265	2	T09211
20	344.5	34.9	198	2	I68897
21	338	34.2	199	2	I52425
22	337.5	34.2	257	2	U00064
23	334	33.8	199	2	A46711
24	334	33.8	576	2	T16005
25	330	33.4	203	2	A12385
26	329.5	33.4	200	2	I51016
27	329	33.3	199	2	A48513
28	324.5	32.9	195	2	UC2258
29	322.5	32.7	271	2	G01790

30	319.5	32.4	183	2	A83983	2-cys peroxidoxi
31	312	31.6	199	2	S73193	hypothetical prote
32	312	31.6	226	2	S43598	mers homolog R075
33	311	31.5	200	2	AB0388	probable alkyl hyd
34	307	31.1	200	2	S76284	hypothetical prote
35	306.5	31.1	180	2	B69867	2-cys peroxidoxi
36	306	31.0	192	2	T41413	thioredoxin peroxi
37	302	30.6	200	2	AB0552	probable peroxidas
38	300	30.4	200	2	G83204	probable peroxidas
39	288	29.2	207	2	E82287	antioxidant, Ahpc/
40	283.5	28.7	195	2	A43858	alkyl hydroperoxid
41	282.5	28.6	196	2	H66587	thio-specific anti
42	282.5	28.6	196	2	E72036	thio-specific anti
43	280	28.4	199	2	F83540	probable alkyl hyd
44	276	28.0	195	2	E87164	alkyl hydroperoxid
45	266	27.0	181	2	AD1275	2-cys peroxidoxi

ALIGNMENTS

```
RESULT 1
JN0289
alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Escherichia coli
N:Alternate names: sulfate starvation-induced protein SS18
C:Species: Escherichia coli
C>Date: 16-Sep-1992 #sequence-revision 30-Sep-1997 #text-change 11-Jun-1999
C:Accession: C64794; JN0289; S78624
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: C64794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-187 <BLAT>
A:Cross-references: GB:AEO00166; GB:U00096; NID:q1786819; PIDN:AC73706.1; PID:q17868
A:Experimental source: strain K-12, substrain MG1655
R:Ueshima, R.; Fujita, N.; Ishihama, A.
Biochem. Biophys. Res. Commun. 184, 634-639, 1992
A:Title: Identification of Escherichia coli proteins cross-reacting with antibodies a
A:Reference number: JN0289; MUID:92246944
A:Accession: JN0289
A:Molecule type: protein
A:Residues: 2-31 <UES>
A>Note: This protein fragment has exact coincidence, except Ile-24, with the first 31
R:Quadrini, M.; Staudenmann, W.; Kertesz, M.; James, P.
Eur. J. Biochem. 239, 773-781, 1996
A:Title: Analysis of global responses by protein and peptide fingerprinting of proteo
coli.
A:Reference number: S78617; MUID:96370830
A:Accession: S78624
A:Molecule type: protein
A:Residues: 2-11 <QUA>
C:Genetics:
A:Gene: ahpc
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
C:Keywords: oxidoreductase
F:2-187/Product: alkyl hydroperoxidase reductase c22 protein #status experimental <MAT>
F:11-146/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match          98.3%  Score 970.5:  DB 2:  Length 187:
Best Local Similarity 99.5%:  Pred. No. 36-81:  0:  Indels  1:  Gaps  1:
Matches 187:  Conservative  0:  Mismatches  0:

OY  1 MSLLNTRKIPFKNQAFKNGEFTETKDEGMSVFFFPADFPVCTELGADVADHE 60
DB  1 MSLLNTRKIPFKNQAFKNGEFTETKDEGMSVFFFPADFPVCTELGADVADHE 59
OY  61 ELQKLGVDVAVSTDTHTTHKAMHSSSEETIAIKYAMIGDPTGALTRNFDNNRDEGLAD 120
DB  61 ELQKLGVDVAVSTDTHTTHKAMHSSSEETIAIKYAMIGDPTGALTRNFDNNRDEGLAD 120
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Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 180
Db 120 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 2
D90709
alkyl hydroperoxide reductase C22 subunit [imported] - Escherichia coli (strain 0157:H7,
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90709
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
NA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA034067.1; PID:g13360102; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECS0644
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 98.3%; Score 970.5; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 3e-81;
Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSLINTKIKPFKNQAKNKEFEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
Db 1 MSLINTKIKPFKNQAKNKEFEITEKDEGRMSV-FFFPADFTFVCPTELGVDADHYE 59
QY 61 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 120
Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 180
Db 120 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 3
H85359
alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Escherichia coli (strain 0157:H
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2001
C:Accession: H85359
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Polamoukis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
A:Cross-references: GB:AE005174; NID:g12513501; PIDN:AGS4940.1; GSPDB:GN00145; UMGCP:207
C:Genetics:
A:Experimental source: strain 0157:H7, substrain EDL933
A:Gene: ahpc

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
C:Keywords: oxidoreductase

Query Match 98.3%; Score 970.5; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 3e-81;
Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSLINTKIKPFKNQAKNKEFEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
Db 1 MSLINTKIKPFKNQAKNKEFEITEKDEGRMSV-FFFPADFTFVCPTELGVDADHYE 59
QY 61 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 120
Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 180
Db 120 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 4
AB0577
alkyl hydroperoxide reductase c22 protein [imported] - Salmonella enterica subsp. ent
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: This species has also been called Salmonella typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB0577
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Plackard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Mout, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AB0577
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05084.1; PID:g16501859; GSPDB:GN00176
C:Genetics:
A:Gene: STY0653
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p

Query Match 97.6%; Score 963.5; DB 2; Length 187;
Best Local Similarity 97.9%; Pred. No. 1.3e-80;
Matches 184; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSLINTKIKPFKNQAKNKEFEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
Db 1 MSLINTKIKPFKNQAKNKEFEITEKDEGRMSV-FFFPADFTFVCPTELGVDADHYE 59
QY 61 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 120
Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 180
Db 120 RATEFVDDPGIIQALTEVTAEGIGRSDSLLRKIKAAQYVAHSGEVCAPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 5
D87610
alkyl hydroperoxide reductase, subunit c [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: D67610
R:Nielsen, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koloro, n.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D67610
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
A:Cross-references: GB:AE005673; NID:913424540; PIDN:AAK24880.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2918
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Query Match 75.2%; Score 742.5; DB 2; Length 187;
Best Local Similarity 72.3%; Pred. No. 2e-60;
Matches 136; Conservative 27; Mismatches 24; Indels 1; Gaps 1;

OY 1 MSLLTKIKPKPNOAKNGEFTIEKDEGRMSVEFFEPADFTFVCPTELDGVADHYE 60
|||||:||||:||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSLLTGLTKPPTAQAYKKGKRYVSADYKGRMSV-FFFTPADFTFVCPTELDADNYD 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 ELQKLGVDVAVSTDTHTFTRKAMHSSSEPTIAKIKYAMIGDPTGALTFRFNDMREDEGLAD 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 VETRLGVEIVAVSTDTHTSRHKAMHSDSPAICKIKRTWGDPSGQVTTNFMELRPVGLAD 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 121 RATEVVDPOGIIQAEIVTAEGIGRDSPLLRKIKAAQYVASHPEGVCPAKWKEGATLAP 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 RGTFLVDPQGVQIQEIVTAEGIGRMAIELLRKIKAAQYVAAHPGEVCPAKWKEGEXTLAP 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 SLDLGVKX 188
|||||:
Db 180 SLDLGVKX 187
|||||:

RESULT 6
GB2668
subunit C of alkyl hydroperoxide reductase X11530 [imported] - Xylella fastidiosa (strain
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: GB2668
R:Anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: GB2668
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <STM>
A:Cross-references: GB:AE003983; GB:AE003849; NID:9106567; PIDN:AAE84339.1; GSPDB:GN00148
R:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
R:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, h
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohna
J.D.; Junqueira, M.L.; Kempf, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigret
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Pa
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaka
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vetore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
C:Gene: XF1530

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 19, 2002, 00:31:21 ; Search time 40.11 Seconds

(without alignments)
181,483 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987

Sequence: 1 MSLLMTKIKPFKNQAFKNKE.....AKKKEGATLAPSLDVCKI 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	965.5	97.8	186	1	AHPC_ECOLI
2	958.5	97.1	186	1	AHPC_SALTY
3	677.5	68.6	187	1	AHPC_BACSU
4	624.5	63.3	168	1	YNDH_BACSP
5	366.5	37.1	266	1	BAS1_ARATH
6	362	36.7	210	1	BAS1_WHEAT
7	361	36.6	198	1	PDX2_RAT
8	361	36.6	210	1	BAS1_HORVU
9	358.5	36.3	198	1	PDX2_MOUSE
10	354	35.9	265	1	BAS1_SPIOI
11	346.5	35.1	256	1	PDX3_HUMAN
12	343.5	34.8	199	1	PDX2_HUMAN
13	338	34.2	199	1	PDX1_RAT
14	337.5	34.2	257	1	PDX3_MOUSE
15	335.5	34.0	257	1	PDX3_BOVIN
16	334	33.8	199	1	PDX1_HUMAN
17	330.5	33.5	199	1	TDX2_BRUMA
18	329.5	33.4	200	1	TDX1_CYNXP
19	329	33.3	199	1	PDX1_MOUSE
20	322.5	32.7	271	1	PDX4_HUMAN
21	322	32.6	229	1	TDX1_BRUMA
22	321.5	32.6	274	1	PDX4_MOUSE
23	312	31.6	199	1	YC42_PORPU
24	312	31.6	226	1	TDX1_CAREL
25	307	31.1	200	1	Y755_SYNY3
26	305.5	31.0	199	1	TDX1_CYNXP
27	291.5	29.5	194	1	TDX1_FASHF
28	291	29.5	200	1	TDX1_ONCMY
29	285.5	28.9	196	1	TSAL_CANAL
30	266	27.0	233	1	CR29_ENTRI
31	265.5	26.9	178	1	R20K_CLOPA
32	262	26.5	204	1	YC42_ODOSI
33	258.5	26.2	195	1	YSA2_YEAST

34	250.5	25.4	195	1	TSAL_YEAST
35	249.5	25.3	197	1	TSAL_BUCAI
36	243.5	24.7	127	1	PX2A_PIG
37	241	24.4	198	1	TSAL_HELPJ
38	241	24.4	198	1	TSAL_HELPJ
39	226.5	22.9	215	1	TDXH_HELPY
40	226.5	22.9	215	1	TDXH_HELPY
41	223	22.6	216	1	TDXH_HELPY
42	221	22.4	216	1	TDXH_HELPY
43	220.5	22.3	215	1	TDX1_SULME
44	216.5	21.9	215	1	TDXH_ARCPU
45	216.5	21.9	217	1	TDXH_METVA

ALIGNMENTS

RESULT	ID	STANDARD	PRT	186 AA
1	AHPC_ECOLI			
AC	P26427			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (SCRP-23)			
DE	(Sulfate starvation-induced protein 8) (SS18).			
GN	AHPC OR B0605 OR Z0749 OR EC50644.			
OS	Escherichia coli, and			
OS	Escherichia coli O157:H7.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562, 83334;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RC	SMILLIE-D.A., Hayward R.S., Suzuki T., Fujita N., Ishihama A.;			
RT	"Locations of genes encoding alkyl hydroperoxide reductase on the			
RT	physical map of the Escherichia coli K-12 genome.";			
RL	J. Bacteriol. 174:3826-3827(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RC	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.;			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.;			
RA	Gregor J., Davis N.W., Kirkpatrick J.A., Goeden M.A., Rose D.J.;			
RA	Mau B., Shao Y.;			
RL	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.;			
RC	Federung N., Hyman R., Kaiman S., Komp C., Kurd O., Lew H., Lin D.;			
RC	Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;			
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RC	MEDLINE=97061202; PubMed=8905232;			
RA	Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.;			
RA	Ikeno K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.;			
RA	Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.;			
RA	Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.;			
RA	Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.;			
RA	Yano M., Horiuchi T.;			
RT	"A 718-kb DNA sequence of the Escherichia coli K-12 genome			
RT	corresponding to the 12.7-28.0 min region on the linkage map.";			
RL	DNA Res. 3:137-155(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=O157:H7 / EDL933 / ATCC 700927;			
RC	MEDLINE=21074935; PubMed=11206551;			

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postal G., Hackett J., Link S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamovis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.",
RL Nature 409:529-533(2001).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.,
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12.",
RL DNA Res. 8:11-22(2001).
[7]
RP SEQUENCE OF 1-30.
RC MEDLINE=92246944; PubMed=1575737;
RA Ueshima R., Fujita N., Ishihama A.,
RT "Identification of *Escherichia coli* proteins cross-reacting with
RT antibodies against region 2.2 peptide of RNA polymerase sigma
RT subunit.",
RL Biochem. Biophys. Res. Commun. 184:634-639(1992).
[8]
RP SEQUENCE OF 1-13.
RC STRAIN-K12 / W3110;
RA Pasquali C., Sanchez J.-C., Xavier F., Golaz O., Hughes G.J.,
RA Fruhlinger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,
RL Hochstrasser D.F.,
RT Submitted (SEP-1994) to the SWISS-PROT data bank.
[9]
RP SEQUENCE OF 1-27 AND 69-80.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.,
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of *Escherichia coli* K-12.",
RL Electrophoresis 18:1259-1313(1997).
[10]
RP SEQUENCE OF 1-20.
RC STRAIN-K12;
RX MEDLINE=96081923; PubMed=7499381;
RA Cha M.-K., Kim H.-K., Kim I.-H.,
RT "Thioredoxin-linked 'thiol peroxidase' from periplasmic space of
RT *Escherichia coli*.",
RL J. Biol. Chem. 270:28635-28641(1995).
[11]
RP SEQUENCE OF 1-10.
RC STRAIN-K12 / MC4100;
RX MEDLINE=96370830; PubMed=8774726;
RA Quadroni M., Staudenmann W., Kertesz M., James P.,
RT "Analysis of global responses by protein and peptide fingerprinting
RT of proteins isolated by two-dimensional gel electrophoresis.
RT Application to the sulfate-starvation response of *Escherichia coli*.",
RL Eur. J. Biochem. 239:773-781(1996).
[12]
RP FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
CC DITHIOL FORM.
[13]
RP SUBUNIT: HOMODIMER (BY SIMILARITY).
[14]
RP THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
CC BY THIOREDOXIN.
[15]
RP SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
[16]
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D13187; BAA02485.1; -
DR EMBL: AE000166; AAC73706.1; -
DR EMBL: U82598; AAB40806.1; -
DR EMBL: D90702; BAA35244.1; -
DR EMBL: D90701; BAA35235.1; -
DR EMBL: AE005240; AAG54940.1; -
DR EMBL: AP002552; BAB34067.1; -
DR PIR: JN0289; JN0289.
DR HSP: P30041; IPRX.
DR SWISS-2DPAGE: P26427; COLI.
DR ECODBASE: B020.9; 6TH EDITION.
DR Ecogene: EC1384; Ahpc.
DR InterPro: IPR000665; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
KW Oxidoreductase; Complete proteome.
FT INIT_MET 0 0
FT ACT_SITE 46 46 BY SIMILARITY.
FT ACT_SITE 165 165 BY SIMILARITY.
SQ SEQUENCE 186 AA; 20630 MW; 40CDA2D344CAl96B CRC64;

Query Match 97.8%; Score 965.5; DB 1; Length 186;
Best Local Similarity 99.5%; Pred. No. 7.9e-80;
Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SLINTKIRKPKKNAFNGEFTETKDTGEGSVFFFFYPADFTFCPELGDVAHYRE 61
DB 1 SLINTKIRKPKKNAFNGEFTETKDTGEGSV-FFFPADFTFCPELGDVAHYRE 59
QY 62 LOKLGVAVYAVSDTHFTKAWHSSSETIYAKIYAMIGDPTGALTRNPNMREDEGLADR 121
DB 60 LOKLGVAVYAVSDTHFTKAWHSSSETIYAKIYAMIGDPTGALTRNPNMREDEGLADR 119
QY 122 AFVVDPOGIIQAEVTAIGRDSADLRLKIKAAQYVASHPEVCAPAKWKEGEATLAPS 181
DB 120 AFVVDPOGIIQAEVTAIGRDSADLRLKIKAAQYVASHPEVCAPAKWKEGEATLAPS 179
QY 182 LDLVKKI 188
DB 180 LDLVKKI 186

RESULT 2
AHPC_SALTY STANDARD; PRT; 186 AA.
AC AHPC_SALTY
AC P19479;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ALKYL hydroperoxide reductase C22 protein (EC 1.6.4.-).
GN AHPC OR STM0608 OR STY0653.
OS *Salmonella typhimurium*.
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC *Salmonella*.
OX NCBI_Taxid=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S. typhimurium; STRAIN-TN1379;
RX MEDLINE=90285183; PubMed=2191951;
RA Tarrapija L.A., Storz G., Brodsky M.H., Lai A., Ames B.N.,
RT "Alkyl hydroperoxide reductase from *Salmonella typhimurium*. Sequence
RT and homology to chlorodoxin reductase and other flavoprotein
RT disulfide oxidoreductases.",
RL J. Biol. Chem. 265:10535-10540(1990).
[2]
RP REVISIONS TO C-TERMINUS.
RC SPECIES-S. typhimurium;
RX MEDLINE=94316629; PubMed=8041738;

RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian
 RT brain: alkyl hydroperoxide reductase and thiol-specific antioxidant
 RT define a large family of antioxidant enzymes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 RL [3]
 RN
 RP SEQUENCE FROM N.A.
 RC MEDLINE-21534948; PubMed-11677609; / SCS01412 / ATCC 700720;
 RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 RN [4]
 RP SEQUENCE OF 1-20 FROM N.A.
 RC SPECIES-S. typhimurium;
 RX MEDLINE-90133925; PubMed-2693740;
 RA Tartaglia L.A., Storz G., Ames B.N.;
 RT "Identification and molecular analysis of oxyR-regulated promoters
 RT important for the bacterial adaptation to oxidative stress.";
 RL J. Mol. Biol. 210:709-719(1989).
 RN [5]
 RP SEQUENCE OF 1-24.
 RC SPECIES-S. typhimurium; STRAIN-OXYR1;
 RX MEDLINE-89109157; PubMed-2643600;
 RA Jacobson F.S., Morgan R.W., Christman M.F., Ames B.N.;
 RT "An alkyl hydroperoxide reductase from *Salmonella typhimurium*
 RT involved in the defense of DNA against oxidative damage. Purification
 RT and properties.";
 RL J. Biol. Chem. 264:1488-1496(1989).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S. typh1; STRAIN-CT18;
 RX MEDLINE-21534947; PubMed-11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typh1 CT18.";
 RL Nature 413:848-852(2001).
 CC
 CC -1- FUNCTION: DIRECTLY REDUCES ALKYL HYDROPEROXIDES WITH THE USE OF
 CC ELECTRONS DONATED BY THE 57 KDA FLAVOPROTEIN ALKYL HYDROPEROXIDE
 CC REDUCTASE.
 CC
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC
 CC -1- PTM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H2O2(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDUXIN.
 CC
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC
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 CC
 CC
 CC EMBL: J05473; AAA16431.1; -;
 CC EMBL: AE008724; AAL19559.1; -;
 CC EMBL: AL627267; CAD05084.1; -;
 CC PIR: A35441; A35441.
 CC PIR: S07525; S07525.

DR HSP: P30041; 1PRX.
 DR Styene: SG10004; ahpc.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 DR Oxidoreductase: Complete proteome.
 RM INIT MET 0 0
 FT ACT SITE 46 46 BY SIMILARITY.
 FT ACT SITE 165 165 BY SIMILARITY.
 FT CONFLICT 1 1 S -> G (IN REF. 5).
 FT CONFLICT 4 4 N -> D (IN REF. 5).
 FT CONFLICT 13 13 Q -> N (IN REF. 5).
 FT CONFLICT 16 16 K -> H (IN REF. 5).
 FT CONFLICT 19 19 E -> H (IN REF. 5).
 FT CONFLICT 22 22 E -> S (IN REF. 5).
 SQ SEQUENCE 186 AA; 20616 MW; 83D48A7A667F5DB0 CRC64;
 Query Match 97.1%; Score 958.5; DB 1; Length 186;
 Best Local Similarity 97.9%; Pred. No. 3.4e-79;
 Matches 183; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
 QY 2 SLINIKIKPFKNQARKNGFEIITEKDTBGRNSVFFFPADFTYCPTELDVADHYEE 61
 DB 1 SLINIKIKPFKNQARKNGFEIITEKDTBGRNSV-FFFPADFTYCPTELDVADHYEE 59
 QY 62 LKLGVDYAVSGTDFHTKAMHSSEETAKIKYAMIGPTGALRPNFNMREDEGLADR 121
 DB 60 LKLGVDYAVSGTDFHTKAMHSSEETAKIKYAMIGPTGALRPNFNMREDEGLADR 119
 QY 122 ATFFVDPQGIQAEVTAEGIGRSDLLRK1KAAQYVAHSGEVCAPAKWKEGATLAPS 181
 DB 120 ATFFVDPQGIQAEVTAEGIGRSDLLRK1KAAQYVAHSGEVCAPAKWKEGATLAPS 179
 QY 182 LDLVGKI 188
 DB 180 LDLVGKI 186
 RESULT 3
 AHP_C_BACSU STANDARD; PRT; 187 AA.
 ID AHP_C_BACSU P80239; P53562;
 AC P80239; P53562;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (General stress
 DE protein 22).
 GN AHP_C.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_Taxid=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Kashara Y., Nakai S., Yoshikawa H., Ogasawara N.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-41.
 RC STRAIN-168 / YB886;
 RX MEDLINE-94236234; PubMed-8180695;
 RA Hartford O.M., Dows B.C.A.;
 RT "Isolation and characterization of a hydrogen peroxide resistant
 RT mutant of *Bacillus subtilis*.";
 RL Microbiology 140:297-304(1994).
 RN [3]
 RP SEQUENCE OF 1-14.
 RC STRAIN-IS58;
 RX MEDLINE-94282319; PubMed-8012595;
 RA Voelker U., Engelmann S., Maul B., Rietdorf S., Voelker A.,
 RA Schmidt R., Mach H., Hecker M.;
 RT "Analysis of the induction of general stress proteins of *Bacillus*
 RT subtilis.";

RL Microbiology 140:741-752(1994).
CC -1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
CC DITHIOL FORM.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS AND
CC GLUCOSE LIMITATION.
CC -1- PTM: THE CYS-47-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-47 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-166-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
CC BY THIOREDOXIN.
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC -----
DR EMBL: D78193; BAA11268.1; -
DR EMBL: 299124; CAB16046.1; -
DR Subtilist; BG11385; ahpc.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
KW Oxidoreductase; Heat shock; Complete proteome.
FT ACT_SITE 47 47 BY SIMILARITY.
FT ACT_SITE 166 166 BY SIMILARITY.
FT CONFLICT 2 2 MISSING (IN REF. 3).
FT CONFLICT 8 8 V->VV (IN REF. 3).
SQ SEQUENCE 187 AA; 20627 MW; 10DF6643BC90F54E CRC64;

Query Match 68.6%; Score 677.5; DB 1; Length 187;
Best Local Similarity 64.9%; Pred. No. 5.9e-54;
Matches 122; Conservative 32; Mismatches 33; Indels 1; Gaps 1;

QY 1 MSLLTRKINPFRNKAQKNEFEITEKDEGRMSVFEFFYPADFTFCVCTELGADVADHYE 60
DB 1 MSLLGKEVLPFAKAKFKNEFIDYTNEDLKQMSV-FCYPPADFSVCTELEDDLOEQYA 59
QY 61 ELQKLGVDVAVSTDTHTFHAKMHSSSETIAKIKYAMIDCPGALTRFNDNREDEGLAD 120
DB 60 AAKELGVEYVSVSTDTHTFHAKMHSSSEKISKITYAMIDPSQITSRNDVDEETGLAD 119
QY 121 RAFFVVDPOGIIQATLEVTAEIGIGIPDASDLRKIKAAQYVASHGFCVCPAKMKEGEATLAP 180
b 120 RGTFTIDPGVAYQYVEINAGIGIGRNASNLVKNKAAQYVRONPGEVCPAKMEGGETLTP 179
QY 181 SLDLVGKI 188
DB 180 SLDLVGKI 187

RESULT 4
YNDH_BACSP STANDARD: PRT; 168 AA.
AC P26830;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in NDH 5' region (Fragment).
OS Bacillus sp. (strain YN-1).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92011449; PubMed=1917890;
RA Xu X., Koyama N., Cui M., Yamagishi A., Nosoh Y., Oshima T.;
RT "Nucleotide sequence of the gene encoding NADH dehydrogenase from an
alkalophilic, Bacillus sp. strain YN-1.";

RL J. Biochem. 109:678-683(1991).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- PTM: THE CYS-28-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-28 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-147-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
CC BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D10701; BAA01544.1; -
DR PIR: PS0179; PS0179.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
KW Hypothetical protein; Antioxidant.
FT NON_TER 1 1
FT ACT_SITE 28 28 BY SIMILARITY.
FT ACT_SITE 147 147 BY SIMILARITY.
SQ SEQUENCE 168 AA; 18479 MW; 2D58C57BB7726CDE CRC64;

Query Match 63.3%; Score 624.5; DB 1; Length 168;
Best Local Similarity 67.5%; Pred. No. 3e-49;
Matches 114; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 20 EFLEITEKDEGRMSVFEFFYPADFTFCVCTELGADVADHYEELQKGVAVSTDTHT 79
DB 1 EFLEISESEFKQMSV-LCTFPADFTFCVCTELEDDLOEYALKEVGEVFSASTDHT 59
QY 80 HKAMHSSSETIAKIKYAMIDCPGALTRFNDNREDEGLADRAATVVPQGIQAEVYA 139
DB 60 HKGWHDSSSTIKITYAMIDGPSQTLRSNFVDLNEVSGLDAGTFLIDPDGVVQAAEINA 119
QY 140 EIGIRASDLKIRAAQYVASHGFCVCPAKMKEGEATLAPSLDVGKI 188
DB 120 EIGIRASDLKIRAAQYVASHGFCVCPAKMKEGEATLAPSLDVGKI 168

RESULT 5
BAS1_ARATH STANDARD: PRT; 266 AA.
AC Q96291; P92938; Q957Y0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 2-cys peroxidoredoxin BAS1, chloroplast precursor.
GN BAS1 OR AT3G11630 OR T19F11.3 OR F24R9.28.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Baler M., Dietz K.-J.;
RT "2-Cys peroxidoredoxin bas1 from Arabidopsis thaliana.";
RL (in) Plant Gene Register PER96-031.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=97408940; PubMed=9263459;
RA Baler M., Dietz K.-J.;
RT "The plant 2-cys peroxidoredoxin BAS1 is a nuclear-encoded chloroplast
protein: its expressional regulation, phylogenetic origin, and
implications for its specific physiological function in plants.";

DR InterPro: IPR000866; AnPc-TSA.
 Dr Pfam: PF00578; AnPc-TSA.
 KW Antioxidant; Chloroplast; Transit peptide.
 FT TRANSIT 1 65 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 66 266 2-CYS PEROXIREDOXIN BAS1.
 FT ACT SITE 119 119 BY SIMILARITY.
 FT ACT SITE 241 241 BY SIMILARITY.
 FT CONFLICT 83 83 E -> K (IN REF. 1).
 FT CONFLICT 101 101 I -> N (IN REF. 1 AND 2).
 FT CONFLICT 122 122 MISSING (IN REF. 1).
 FT CONFLICT 192 192 I -> IGI (IN REF. 2).
 FT CONFLICT 233 235 IOE -> TG (IN REF. 1).
 FT CONFLICT 247 247 P -> S (IN REF. 1).
 SQ SEQUENCE 266 AA; 29092 MW; 2CEBA76A1A8654AD CRC64;

Query Match 37.1%; Score 366.5; DB 1; Length 266;
 Best Local Similarity 37.7%; Pred. No. 7.7e-26;
 Matches 69; Conservative 39; Mismatches 72; Indels 3; Gaps 1

QY 1 MSLNFKIKPKFNQAFKNGEIEITEKDTGKMSVFFFPADFTVCPTELGDVADHYE 60
 Db 72 LPLVGNKAPDEAEAVFQDFEFKVLSDYICKKKVYLFFPDPFTFVCPTETLAFSDRHS 131
 QY 61 ELQKGVGVVANSPTGHTHTKAW---HSSSEIARIKIKYAMIDPGALIRNPNMDEDS 117
 Db 132 EPEKNTETVLGVSVDVSFSLAMVOTDRKSGGLGDLNPLISDYTKSISKSGVLIHDOG 191
 QY 118 LADRAFPVDPQGIQALAEVTEAGIGRPSDGLRKIKAAQVAAHSHPGECAPAKKKEGAT 177
 Db 192 IALRGLFTIIDEGVLIQHSITNNLNGIGRSVDENRMLQALQYIQENDEVCAPAKKKEGNS 251

QY 178 LAP 180
 Db 252 MKP 254

RESULT 6
 BAS1_WHEAT
 ID BAS1_WHEAT STANDARD; PRT; 210 AA.
 AC P80602;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2-cys peroxiredoxin BAS1, chloroplast precursor (Thiol-specific
 antioxidant protein) (Fragment).
 GN TSA.
 OS Triticum aestivum (Wheat).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NORIN 61; TISSUE=Seedling;
 RA Tsunoyama Y., Toyoshima Y.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 11-35.
 RC STRAIN=CV. NOURIN 61; TISSUE=leaf;
 RA Tsunoyama Y., Takashi S., Toyoshima Y.;
 RL Submitted (MAY-1996) to the SWISS-PROT data bank.
 CC -1- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE
 CC DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- PM: THE CYS-64-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H2O2(2). AND THE OXIDIZED CYS-64 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-185-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AnPc/TSA FAMILY.

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DR EMBL: AB000405; BAA19099.1; -
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Chloroplast; Transit peptide.
 FT TRANSIT 1 10 CHLOROPLAST.
 FT CHAIN 11 210 2-CYS PEROXIREDOXIN BAS1.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 185 185 BY SIMILARITY.
 SQ SEQUENCE 210 AA; 23326 MW; E2D488179D6937E6 CRC64;

Query Match 36.7%; Score 362; DB 1; Length 210;
 Best Local Similarity 38.3%; Pred. No. 1.5e-25;
 Matches 70; Conservative 37; Mismatches 72; Indels 4; Gaps 2;

QY 1 MSLLNTKIKPFKNQAFKNGEIEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
 DB 17 LPLVGNKADPFAAEVDFDEFINVKLSYIGKKYVLFEPYDFTEVCPTEITAFSDRHE 76
 QY 61 ELQKLGVDYVNSTDHFTHKAM---HSSSETIAKKIKYAMIGDPTGALTRFNDNMRDEBG 117
 DB 77 EEKINTEILGVSVDVSHLAWQTERKSGGLGDKYPLVSVTKSISKSGVLLIPDGG 136
 QY 118 LADRAFVVDPOGIIQAEIVTAEGIGRSDSLRLKIKAAQYVASHGECAPAKKKEGEAT 177
 DB 137 IALRGFIIDKRGVIOHSTINNLGIGRSVDLRTLRALQYV-KRDEVCPAGWKKEGNS 195
 QY 178 LAP 180
 DB 196 MKP 198

RESULT 7
 PDX2_RAT STANDARD; PRT; 198 AA.
 AC P35704;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 GN Peroxiredoxin 2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent
 GN peroxidase reductase 1) (Thiol-specific antioxidant protein) (TSA).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94316629; PubMed=8041738;
 RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian
 RT brain: alkyl hydroperoxide reductase and thiol-specific antioxidant
 RT define a large family of antioxidant enzymes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 CC -!- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
 CC THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
 CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
 CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
 CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
 CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
 CC CONCENTRATIONS OF H(2)O(2).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED. UPON OXIDATION (BY

CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

DR EMBL: U06099; AAA19959.1; -
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant.
 FT ACT_SITE 51 51 BY SIMILARITY.
 FT ACT_SITE 172 172 BY SIMILARITY.
 SQ SEQUENCE 198 AA; 21784 MW; FC6AD9B0E9C4447B CRC64;

Query Match 36.6%; Score 361; DB 1; Length 198;
 Best Local Similarity 40.3%; Pred. No. 1.7e-25;
 Matches 73; Conservative 35; Mismatches 65; Indels 8; Gaps 4;

QY 9 KP---FKNAFKNGEIEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYEELQKL 65
 DB 10 KRAPDPTGAIVADVADAKKEIKLSDYRK-VLFEPYDFTEVCPTEITAFSDHAEFRLL 68
 QY 66 GVDYVAVSTDTHTFKAMHSSSET---IAKKIKYAMIGDPTGALTRFNDNMRDEGLADRA 122
 DB 69 GCEVLGVSVDQSOTHLAWINTPRKEGLGPLNPLADVTKSLSONYGVAKNDGEIAYNG 128
 QY 123 TFFVDDPOGIIQAEIVTAEGIGRSDSLRLKIKAAQYVASHGECAPAKKKEGEATLAPSL 182
 DB 129 LFLIDAKGVLRQITVNDLDFVGRSVDEALRLVQAFQYTTDEH-GEVCPAGKPGSDITIKPAV 187
 QY 183 D 183
 DB 188 D 188

RESULT 8
 BAS1_HORVU STANDARD; PRT; 210 AA.
 AC Q96468;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 GN 2-cys peroxiredoxin BAS1, chloroplast precursor (Thiol-specific
 GN antioxidant protein) (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GERBEL; TISSUE=leaf;
 RX MEDLINE=96382424; PubMed=8790288;
 RA Balier M., Dietz K.-J.;
 RT "Primary structure and expression of plant homologues of animal and
 RT fungal thioredoxin-dependent peroxide reductases and bacterial alkyl
 RT hydroperoxide reductases.";
 RL Plant Mol. Biol. 31:553-564(1996).
 CC -!- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IMPORTANT IN

CC THE DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LEAF BLADE, SHEATH, BASTIPLAST,
CC STEM AND GREEN SPIKE. MAXIMAL EXPRESSION IN YOUNG DEVELOPING
CC SHOOT SEGMENTS WHERE CELL DIVISION AND ELONGATION TAKE PLACE. NOT
CC EXPRESSED IN ROOTS.
CC -1- DEVELOPMENTAL STAGE: MAXIMAL LEVELS ARE SEEN IN 4-DAY OLD
CC SEEDLINGS AND DECLINE DURING AGING OF THE SEEDLING.
CC -1- PTM: THE CYS-64-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-64 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-185-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z34917; CAA84396.1; -.
CC HSSP: P30041; 1PRX.
CC InterPro: IPR000866; Ahpc-TSA.
CC Pfam: PF00578; Ahpc-TSA; 1.
CC Antioxidant; Chloroplast; Transit peptide.
CC NON_TER 1
CC TRANSIT 1
CC CHAIN 1 10 CHLOROPLAST (BY SIMILARITY).
CC ACT_SITE 11 210 2-CYS PEROXIREDOXIN BAS1.
CC ACT_SITE 64 64 BY SIMILARITY.
CC ACT_SITE 185 185 BY SIMILARITY.
CC SEQUENCE 210 AA; 23298 MW; 4DD488179D6BCAC9 CRC64;

Query Match 36.6%; Score 361; DB 1; Length 210;
Best Local Similarity 38.3%; Pred. No. 1.8e-25;
Matches 70; Conservative 37; Mismatches 72; Indels 4; Gaps 2;

OY 1 MSLINTKIKPFKNQAFKNGEFTIEKDEGRMSVFFFPYADFTVCPTGLGVADHYE 60
DB 17 LPLVGNKAPDFAEAFAVDFEDFNKLSIDYIKKYYLFFPYLDFEFTVCPTGLTAFSDRGE 76
OY 61 ELQKGVGVYVYVSTDTFTFKAW---HSSEFTIAKIKYAMIGDPGALTRNDNMREDG 117
DB 77 EEEKINTELGVSDVSFESHLMVOTERKSGGLGDKYPLVDYTKSISKSGVLIPDGG 136
OY 118 LADRAFTFVVDPGIIOAIEVTAEGIGRDASDLLRKIKAAQYVAASHGEGCPAKWKKEGAT 177
DB 137 IALRGLFTIDKRGCVIOHSTINNLGIGRSVDELTRTLQALQYV-KPDEVCPAGWKKEGKS 195
OY 178 LAP 180
DB 196 MKP 198
RESULT 9
PDX2_MOUSE STANDARD: PRT; 198 AA.
AC Q61171; Q60796;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxiredoxin 2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent
DE peroxidase 1) (Thiol-specific antioxidant protein) (TSA).
GN PRDX2 OR TDPX1 OR TPX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE-97238626; PubMed-9115640;
RA Ichimaya S., Davis J.G., O'Rourke D.M., Katsumata M., Greene M.I.;
RT "Murine thioredoxin peroxidase delays neuronal apoptosis and is
RT expressed in areas of the brain most susceptible to hypoxic and
RT ischemic injury.";
RL DNA Cell Biol. 16:311-321(1997).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-129;
RA Oberbauer I.;
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RA Chae H.Z., Kim H., Rhee S.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
CC THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
CC CONCENTRATIONS OF H(2)O(2).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BONE
CC MARROW. HIGH LEVELS ALSO FOUND IN HEART, BRAIN, KIDNEY AND
CC SKELETAL MUSCLE. LOWER LEVELS IN LIVER, LUNG AND THYMUS.
CC -1- PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U51679; AAB01941.1; -.
CC EMBL: X82067; CAA57566.1; -.
CC EMBL: U20611; AAA69475.1; -.
CC HSSP: P30041; 1PRX.
CC SMISS-2DPAGE: O61171; MOUSE.
CC MGD: MGI:109486; Prdx2.
CC InterPro: IPR000866; Ahpc-TSA.
CC Pfam: PF00578; Ahpc-TSA; 1.
CC Antioxidant.
CC ACT_SITE 51 51 BY SIMILARITY.
CC ACT_SITE 172 172 G -> A (IN REF. 3).
CC CONFLICT 97 97 T -> N (IN REF. 3).
CC CONFLICT 182 182
CC SEQUENCE 198 AA; 21778 MW; FE216F5426F7174D CRC64;

Query Match 36.3%; Score 358.5; DB 1; Length 198;
Best Local Similarity 40.3%; Pred. No. 2.8e-25;
Matches 71; Conservative 35; Mismatches 65; Indels 5; Gaps 3;

OY 11 FKNQAFKNGEFTIEKDEGRMSVFFFPYADFTVCPTGLGVADHYEELQKGVYV 70
DB 15 FATAVVDGAFKIKSDYRGKY-VLFFPYLDFEFTVCPTGLTAFSDHAEPRKIGCEVL 73
OY 71 AVSTDTFTFKAWHSSEF---IAKIKYAMIGDPGALTRNDNMREDGLADRAFTVVD 127
DB 74 GVSVDQSFTHLAWINTPRREGIGLPLPLADVTKSLSQNGVGLKNDEGIAYRGLFTLD 133

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CC -----
CC EMBL: D49396; BA08389.1;
DR EMBL: BC002685; AA02685.1;
DR EMBL: T10952; NOT_ANNOTATED_CDS.
DR HSSP: P30041; IPRX.
DR SWISS-2DPAGE: P30048; HUMAN.
DR SIENA-2DPAGE: P30048;
DR MIM: 604769;
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA.1.
KW Antioxidant; Mitochondrion; Transit peptide.
FT TRANSIT 1 62 MITOCHONDRION.
FT CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
FT ACT_SITE 108 108 BY SIMILARITY.
FT ACT_SITE 229 229 BY SIMILARITY.
SQ SEQUENCE 256 AA; 27692 MW; 8BBB/F5E5BFE9BE CRC64;

Query Match 35.1%; Score 346.5; DB 1; Length 256;
Best Local Similarity 40.2%; Pred. No. 4.6e-24;
Matches 70; Conservative 33; Mismatches 66; Indels 5; Gaps 3;

OY 11 FKNQAFKNGEFTETKEDTEGRHVSFFFPADFTFCPTLEDVADHYEELQKLGVDY 70
DB 72 FKGTAIVNGEFDLSDPFKQKYL-LFFYPLDFTFCPTLEIVASDKANEFHDVNCVY 130
OY 71 AVSTDTHTTKAHSSSET---IAKIKYAMICDPGALTRFNDNMREDEGLADRTFVVD 127
DB 131 AVSVSHSHSLAMINTPRKNGIGLMNTALSDLTQISRDYGLVLEGSLALRGIFID 190
OY 128 PGQIQAIEVTEAGIGRSDSLRRIKAAQYVASHPEVCPRKMEGERTLAPS 181
DB 191 PNGVILKHSVNDLPVGRSVYEETRLVKAFQYVETH-GEVCPANMTPDSEPTIPS 243

RESULT 12
PDX2_HUMAN STANDARD: PRT: 198 AA.
ID P32119; P35701; P31945; Q92763;
AC P32119; P35701; P31945; Q92763;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxisomal 2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxidase reductase 1) (Thiol-specific antioxidant protein) (TSA) (PRP) (Natural killer cell enhancing factor B) (NKEF-B).
DE PRDX2 OR TDPX1 OR NKEFB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-94193012; PubMed-814038;
RX Lim Y.-S., Cha M.-K., Kim H.-K., Kim I.-H.;
RT "Type thiol-specific antioxidant protein from human brain: gene cloning and analysis of conserved cysteine regions.";
RL Gene 140:279-284(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE-94299283; PubMed-8026862;
RX Shau H., Butterfield L.H., Chiu R., Kim A.;
RT "Cloning and sequence analysis of candidate human natural killer-enhancing factor genes.";
RL Immunogenetics 40:129-134(1994).
RN [3]
RN SEQUENCE OF 35-198 FROM N.A.
RA Oberbauer I.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE OF 17-25; 140-150 AND 163-185.
RC TISSUE=Keratinocytes;

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RX MEDLINE-93162043; PubMed-1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [5]
RN SEQUENCE OF 17-26 AND 93-103.
RC TISSUE=Erythrocyte;
RX MEDLINE-94147970; PubMed-8313871;
RX Golaz O., Hughes G.J., Frutiger S., Paquet N., Balroch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
RN [6]
RN SEQUENCE OF 17-26; 111-135 AND 140-157.
RC TISSUE=Colon carcinoma;
RX MEDLINE-97295306; PubMed-9150948;
RX Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR CONCENTRATIONS OF H(2)O(2).
CC -1- FUNCTION: ENHANCES NATURAL KILLER (NK) CELLS ACTIVITY.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-SOH) RAPIDLY REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE REDUCED BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHC/TSA FAMILY.
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CC -----
CC EMBL: 222548; CA80269.1;
DR EMBL: L19185; AA50465.1;
DR EMBL: X82321; CA57764.1;
DR HSSP: P30041; IPRX.
DR SWISS-2DPAGE: P32119; HUMAN.
DR Aarhus/Ghent-2DPAGE: 6116; IEF.
DR MIM: 600538;
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA.1.
KW Antioxidant.
FT ACT_SITE 51 51 BY SIMILARITY.
FT ACT_SITE 172 172 BY SIMILARITY.
FT ACT_SITE 59 66 SNRADERF -> TTVKRTSA (IN REF. 1).
FT CONFLICT 82 82 T -> N (IN REF. 2).
FT CONFLICT 105 105 A -> G (IN REF. 2).
FT CONFLICT 120 120 T -> N (IN REF. 1).
FT CONFLICT 175 175 G -> A (IN REF. 1).
FT CONFLICT 180 180 S -> R (IN REF. 1).
SQ SEQUENCE 198 AA; 21892 MW; 1AC781D908B3B46 CRC64;

Query Match 34.8%; Score 343.5; DB 1; Length 198;
Best Local Similarity 38.7%; Pred. No. 6.3e-24;
Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

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DR MGD: MGI:88034; Prdx3.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA.1.
 KM Antioxidant; Mitochondrion; Transit peptide.
 FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
 FT ACT_SITE 109 109 BY SIMILARITY.
 FT ACT_SITE 230 230 BY SIMILARITY.
 SQ SEQUENCE 257 AA; 28127 MW; 66513f2c5f1d56c0 CRC64;

Query Match 34.2%; Score 337.5; DB 1; Length 257;
 Best Local Similarity 38.5%; Pred. No. 3e-23;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFTETKEDTGRMSYFFFPYPADFTFVCPTLGDVADHYEELQKLGVDY 70
 DB 73 FKGTAIVNGEFTETKEDTGRMSYFFFPYPADFTFVCPTLGDVADHYEELQKLGVDY 131

QY 71 AVSTDTHTFKAMHSSSET---IAKIKYAMIDPGALTRFNDNMRDEGLADRATFYVD 127
 DB 132 AVSVSHFSLAWINTPRKNGSLGHMNTLLSDITKQISRDYGLLESGIALRGIFITD 191

QY 128 PGGITIAIEVTAEIGGRDASDLRLKRIKAAQYVASHPEGVCAPKMKEGEATLAP 181
 DB 192 PNGVVKHLSVNDLPVGRSVEETLRVKAQFVEYTH-GEVCPANWIPESPTIKPS 244

RESULT 15
 PDX3_BOVIN

ID PDX3_BOVIN STANDARD; PRT; 257 AA.
 AC P35705;

DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Thioredoxin-dependent peroxidase, mitochondrial precursor
 DE (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (SP-22 protein).
 GN PRDX3 OR AOP1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID:9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=97069947; PubMed=8912927;
 RA Hiroi T., Watabe S., Takimoto K., Yago N., Yamamoto Y., Takahashi S.Y.,
 "The cDNA sequence encoding bovine SP-22, a new defence system
 against reactive oxygen species in mitochondria.";
 RL DNA Seq. 6:239-242(1996).
 [2]
 RN SEQUENCE OF 2-257 FROM N.A.

RP TISSUE=Adrenal medulla;
 RX MEDLINE=94375407; PubMed=8089078;
 RA Watabe S., Kohno H., Kouyama H., Hiroi T., Yago N., Nakazawa T.,
 "Purification and characterization of a substrate protein for
 mitochondrial ATP-dependent protease in bovine adrenal cortex.";
 RL J. Biochem. 115:648-654(1994).
 CC -1- FUNCTION: THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE. PROTECTS
 CC RADICAL-SENSITIVE ENZYMES FROM OXIDATIVE DAMAGE BY A RADICAL-
 CC GENERATING SYSTEM.

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
 CC SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- PFM: THE CYS-109-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H2O(2), AND THE OXIDIZED CYS-109 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-230-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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DR EMBL: D82025; BAA11511.1; -.
 DR HSRP: P30041; IPRX.
 DR InterPro: IPR000866; Ahpc-TSA.

DR Pfam: PF00578; Ahpc-TSA.1.
 KM Antioxidant; Mitochondrion; Transit peptide.
 FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
 FT ACT_SITE 109 109 BY SIMILARITY.
 FT ACT_SITE 230 230 BY SIMILARITY.
 SQ SEQUENCE 257 AA; 28195 MW; F2B89EE2F172A42D CRC64;

Query Match 34.0%; Score 335.5; DB 1; Length 257;
 Best Local Similarity 39.9%; Pred. No. 4.5e-23;
 Matches 69; Conservative 33; Mismatches 66; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFTETKEDTGRMSYFFFPYPADFTFVCPTLGDVADHYEELQKLGVDY 70
 DB 73 FKGTAIVNGEFTETKEDTGRMSYFFFPYPADFTFVCPTLGDVADHYEELQKLGVDY 131

QY 71 AVSTDTHTFKAMHSSSET---IAKIKYAMIDPGALTRFNDNMRDEGLADRATFYVD 127
 DB 132 AVSVSHFSLAWINTPRKNGSLGHMNTLLSDITKQISRDYGLLESGIALRGIFITD 191

QY 128 PGGITIAIEVTAEIGGRDASDLRLKRIKAAQYVASHPEGVCAPKMKEGEATLAP 180
 DB 192 PNGVVKHLSVNDLPVGRSVEETLRVKAQFVEYTH-GEVCPANWIPESPTIKPS 243

Search completed: May 19, 2002, 01:58:37
 Job time: 5236 sec

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OM protein - protein search, using sw model

Run on: May 19, 2002, 00:37:01 ; Search time 97.3 Seconds
(without alignments)
334.235 Million cell updates/sec

Title: US-09-679-705-24
Perfect score: 987
Sequence: 1 MSLLNTKIKFKKNGAFKNGE.....AKMKGEATLAPSLDVGKI 188

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_virus:*
- 16: SP_bacteriap:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742.5	75.2	187	16	Q9A4B8
2	719.5	72.9	187	2	082863
3	714	72.3	206	16	Q9PD49
4	687.5	69.7	187	2	Q9KH10
5	662	67.1	188	2	087200
6	644.5	65.3	189	16	Q53647
7	631.5	64.0	188	2	Q9R072
8	629	63.7	186	16	Q99XR7
9	626	63.4	186	2	066265
10	605.5	61.3	187	16	Q916Z3
11	603.5	61.1	187	16	Q9C1L9
12	589.5	59.7	187	2	006464
13	563.5	57.1	187	2	030738
14	488.5	49.5	188	16	083522
15	455.5	46.1	211	16	066779
16	385	39.0	174	17	Q97C80

17	375	38.0	174	17	Q9HLS3	Q9HLS3 thermoplasm
18	370.5	37.5	258	10	081480	081480 seale cere
19	370.5	37.5	271	10	Q9FNM9	Q9FNM9 arabidopsis
20	370.5	37.5	271	10	Q9C5R8	Q9C5R8 arabidopsis
21	370.5	37.5	273	10	Q9FED5	Q9FED5 arabidopsis
22	364.5	36.9	270	10	Q9FUC5	Q9FUC5 brassica na
23	364.5	36.9	275	10	Q9M4P9	Q9M4P9 riccia flui
24	361.5	36.6	199	5	044366	044366 onchocerca
25	358.5	36.3	198	11	Q9CWM4	Q9CWM4 mus musculu
26	355.5	36.0	195	5	Q9N1J8	Q9N1J8 ascaris suu
27	355.5	36.0	199	5	076452	076452 onchocerca
28	353.5	35.8	198	11	088376	088376 mus musculu
29	351.5	35.6	260	10	Q9FEI2	Q9FEI2 phaseolus v
30	349.5	35.4	199	5	016026	016026 dirofilaria
31	346.5	35.1	199	5	044841	044841 onchocerca
32	346.5	35.1	256	4	Q96HK4	Q96HK4 homo sapien
33	345.5	35.0	193	5	Q9G0B2	Q9G0B2 litomosoid
34	345.5	35.0	198	11	Q9DB49	Q9DB49 mus musculu
35	344.5	34.9	199	5	016006	016006 dirofilaria
36	343.5	34.8	263	10	Q93X25	Q93X25 pisum sativ
37	338.5	34.3	199	13	Q9T886	Q9T886 oncorhynch
38	335.5	34.0	185	5	097161	097161 schistosoma
39	334	33.8	576	5	019265	019265 caenorhabdi
40	333.5	33.6	203	2	Q9L3Q5	Q9L3Q5 eubacterium
41	332	33.6	199	6	Q9BG13	Q9BG13 bos taurus
42	331.5	33.6	257	11	Q9Z0V6	Q9Z0V6 rattus norv
43	330.5	33.5	199	10	Q9FMS2	Q9FMS2 chlamydomon
44	330.5	33.5	223	5	Q9B1F6	Q9B1F6 diatomalari
45	330.5	33.5	235	10	Q9FE86	Q9FE86 chlamydomon

ALIGNMENTS

RESULT	ID	Q9A4B8	PRELIMINARY	PRT	187 AA.
AC	Q9A4B8				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DE	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	ALKYL HYDROPEROXIDE REDUCTASE, SUBUNIT C.				
GN	CC2918.				
OS	Caulobacter crescentus.				
OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group.				
OC	Caulobacter.				
OX	NCBI_TaxID=69394;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 19089 / CB15;				
RX	MEDLINE=21173698; PubMed=11259647;				
RA	Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,				
RA	Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,				
RA	Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,				
RA	DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,				
RA	Kolman J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,				
RA	Uterback J., Tran K., Wolf A., Yamathavan J., Ermolaeva M., White O.,				
RA	Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,				
RT	"Complete genome sequence of Caulobacter crescentus."				
RU	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).				
DR	EMBL: AEO05956; AKK24880.1; -				
DR	TIGR: CC2918;				
DR	InterPro: IPR000866; Ahpc-TSA.				
DR	Pfam: PF00578; Ahpc-TSA; 1.				
KW	Complete proteome.				
SQ	SEQUENCE 187 AA; 20627 MW; 3079FAB56293CD37 CRC64;				

Query Match 75.2%; Score 742.5; DB 16; Length 187;
Best Local Similarity 72.3%; Pred. No. 5,4e-61;
Matches 136; Conservative 27; Mismatches 24; Indels 1; Gaps 1;
QY 1 MSLLNTKIKFKKNGAFKNGEIEITEKDTGSRMSVFFFPADPTFCPELGADVADHYE 60

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DB 1 MSLINTEIRPFAQAKDOKFVYSEADYKGNKV-FFFPADFTFVCPTELEDLADNDY 59
QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTRFNDNMRDEGLAD 120
DB 60 VETRLGVEIYAVSTDTHTFKAMHSDSPAIGKIKYTMVGPSPQGVNNEFIMRPGVLAD 119
QY 121 RAEFVVDPOGIIQAEVTAEGIGRDSDLRLKIKAAQYVASHGECVCPAKWKEGATLAP 180
DB 120 RGTFLVDPOGVIOFMETVABGIRNAIELRLKIKAAQYVAAHGEVCPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
DB 180 SLDLVGKI 187

RESULT 2
ID 082863 PRELIMINARY; PRT; 187 AA.
AC 082863;
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 17, Last annotation update)
DE AHPC.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOL;
RA Fukumori F., Horikoshi K.;
RT "Toluene induced Constitutive Overexpression of An Alkyl Hydroperoxide
the ahp genes.";
RT Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010689; BAA31468.1; -.
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 187 AA; 20507 MW; CC6351406B9C8168 CRC64;

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Query Match 72.9%; Score 719.5; DB 2; Length 187;
Best Local Similarity 67.6%; Pred. No. 7.3e-59;
Matches 127; Conservative 34; Mismatches 26; Indels 1; Gaps 1;

QY 1 MSLINTEIRPFAQAKDOKFVYSEADYKGNKV-FFFPADFTFVCPTELEDLADNDY 59
DB 1 MSLINTEIRPFAQAKDOKFVYSEADYKGNKV-FFFPADFTFVCPTELEDLADNDY 59
QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTRFNDNMRDEGLAD 120
DB 60 EFKLGEVETVSTDTHTFKAMHSDSPAIGKIKYTMVGPSPQGVNNEFIMRPGVLAD 119
QY 121 RAEFVVDPOGIIQAEVTAEGIGRDSDLRLKIKAAQYVASHGECVCPAKWKEGATLAP 180
DB 120 RGTFLVDPOGVIOFMETVABGIRNAIELRLKIKAAQYVAAHGEVCPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
DB 180 SLDLVGKI 187

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RESULT 3
ID 09PD49 PRELIMINARY; PRT; 206 AA.
AC 09PD49;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SUBUNIT C OF ALKYL HYDROPEROXIDE REDUCTASE.
SQ

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GN XF1530.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group.
OX Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin J.M., Britones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frome M., Furlan L.R.,
RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Zeldanis J., Zetubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003983; AAF84339.1; -.
DR HSSP; P30041; 1PRX.
KW Complete proteome.
SQ SEQUENCE 206 AA; 22891 MW; AF703BDE833698D6 CRC64;

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Query Match 72.3%; Score 714; DB 16; Length 206;
Best Local Similarity 69.1%; Pred. No. 2.7e-58;
Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;

QY 1 MSLINTEIRPFAQAKDOKFVYSEADYKGNKV-FFFPADFTFVCPTELEDLADNDY 59
DB 21 MSVINTELSKATAYKNGQVEVSEAVLKKMAY-FVFPADFTFVCPTELEDLADNDY 79
QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTRFNDNMRDEGLAD 120
DB 80 EFKLGEVETVSTDTHTFKAMHSDSPAIGKIKYTMVGPSPQGVNNEFIMRPGVLAD 119
QY 121 RAEFVVDPOGIIQAEVTAEGIGRDSDLRLKIKAAQYVASHGECVCPAKWKEGATLAP 180
DB 139 RGTFLVDPOGVIOFMETVABGIRNAIELRLKIKAAQYVAAHGEVCPAKWKEGATLAP 179
QY 181 SLDLVGKI 188
DB 199 SLDLVGKI 206

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RESULT 4
ID 09KH10 PRELIMINARY; PRT; 187 AA.
AC 09KH10;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PEROXIREDOXIN.
SQ

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QY 59 YEELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTNRDNKREDEGL 118
 DB 60 YEELQKLGVDYAVSTDTHTFKAMHSDAISKITTYMIGDPTGALTNRDNVDEATGL 119
 QY 119 ADRAITFVVDQGIQAEVTAEGIGRSDSLRKIKAAOYVASHPEVCAPKMEGEATL 178
 DB 120 AORCTFTIDPDGVVQAEINADGIGRSDSLRKIKAAOYVASHPEVCAPKMEGEATL 179
 QY 179 APSLDLVGKI 188
 DB 180 QPGLDLVGKI 189
 RESULT 7
 Q9R072 PRELIMINARY; PRT; 188 AA.
 AC Q9R072: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 RT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 GN ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.
 OS Bacteroides fragilis.
 OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
 OX NCBI_TaxID=817;
 RN SEQUENCE FROM N.A.
 RC STRAIN=638R;
 RX MEDLINE=99412269; PubMed=10482511;
 RA Rocha E.R., Smith C.J.;
 RT Role of the alkyl hydroperoxide reductase (ahpC) gene in oxidative
 stress defense of the obligate anaerobe Bacteroides fragilis.";
 RL J. Bacteriol. 181:5701-5710(1999).
 DR EMBL; AF129406; AAD52147.1; -
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PR00578; Ahpc-TSA; 1.
 SQ SEQUENCE 188 AA; 21061 MW; 4A474FF66D6C614 CRC64;

Query Match 64.0%; Score 631.5; DB 2; Length 188;
 Best Local Similarity 60.8%; Pred. No. 1e-50;
 Matches 113; Conservative 38; Mismatches 34; Indels 1; Gaps 1;
 QY 3 LINTKIKPFKNQAFKNGEIEITEKDTGRMSVFFFPADTFVCPTELGVADHYEEL 62
 DB 4 IINSQMEFVQAFQNSGFKTVSSSEYKGMAL-FFFPADTFVCPTELGVADHYEEL 62
 DB 63 QKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTNRDNKREDEGLADRA 122
 DB 63 QAMGVEYVSTDSHFVHKAMHSDAISKITTYMIGDPTGALTNRDNKREDEGLADRA 122
 QY 123 TFVVDQGIQAEVTAEGIGRSDSLRKIKAAOYVASHPEVCAPKMEGEATLAPSL 182
 DB 123 TFLVNEBGRKIKVAEIQDNNIGRNADELKRVAAQFVAITHDGEVCPAKMKGEATLPST 182
 QY 183 DLVGKI 188
 DB 183 DLVGKI 188
 RESULT 8
 Q99XR7 PRELIMINARY; PRT; 186 AA.
 AC Q99XR7: 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 RT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 GN PUTATIVE ALKYL HYDROPEROXIDASE.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OX NCBI_TaxID=1314;

OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Szatele S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL; AE006628; AAK34732.1; -
 DR Peroxidase; Complete proteome.
 SQ SEQUENCE 186 AA; 20483 MW; 5B7147A476DBAER1 CRC64;

Query Match 63.7%; Score 629; DB 16; Length 186;
 Best Local Similarity 62.2%; Pred. No. 1.8e-50;
 Matches 117; Conservative 28; Mismatches 41; Indels 2; Gaps 2;
 QY 1 MSLINTKIKPFKNQAFKNGEIEITEKDTGRMSVFFFPADTFVCPTELGVADHYEEL 60
 DB 1 MSLIGKEIAPSAQAYHDGKFTVTNEDVKGMAV-FCFPADTFVCPTELGVADHYEEL 59
 QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTNRDNKREDEGLAD 120
 DB 60 TLKSLGVEYVSTDTHTFKAMHSDAISKITTYMIGDPTGALTNRDNVDEATGL 119
 QY 121 RATFVVDQGIQAEVTAEGIGRSDSLRKIKAAOYVASHPEVCAPKMEGEATLAP 180
 DB 119 RGFPIVDPDGIQAEVTAEGIGRSDSLRKIKAAOYVASHPEVCAPKMEGEATLAP 178
 QY 181 SLDLVGKI 188
 DB 179 SLDLVGKI 186

RESULT 9
 O66265 PRELIMINARY; PRT; 186 AA.
 AC O66265: 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 RT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 GN ALKYL HYDROPEROXIDASE.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIB 11723;
 RX MEDLINE=20120090; PubMed=10656297;
 RA Poole L.B., Higuchi M., Shimada M., Li Calzi M., Kamio Y.;
 RT "Streptococcus mutans H202-forming NADH oxidase is an alkyl
 hydroperoxide reductase protein.";
 RL Free Radic. Biol. Med. 28:108-120(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIB 11723;
 RX MEDLINE=95036869; PubMed=7765479;
 RA Higuchi M., Shimada M., Matsumoto J., Yamamoto Y., Rhaman A.,
 RA Kamio Y.;
 RT "Molecular cloning and sequence analysis of the gene encoding the
 H202-forming NADH oxidase from Streptococcus mutans.";
 RL Biosci. Biotechnol. Biochem. 58:1603-1607(1994).
 DR EMBL; AB010712; BAA25695.1; -
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PR00578; Ahpc-TSA; 1.
 DR Peroxidase.
 SQ SEQUENCE 186 AA; 20478 MW; 1C7E9BEA4D739F06 CRC64;

[illegible]

	RESULT	12	
	006464		
ID	006464	PRELIMINARY;	PRT; 187 AA.
AC	006464;		
DT	01-JUL-1997	(TRMBLrel, 04, Created)	
DT	01-JUL-1997	(TRMBLrel, 04, Last sequence update)	
DT	01-DEC-2001	(TRMBLrel, 19, Last annotation update)	
DE	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.		
GN	AHPc.		
OS	Xanthomonas campestris (pv. phaseoli).		
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;		
OC	Xanthomonas.		
OX	NCBI_TaxID=29445;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PHASEOLI;		
RX	MEDLINE=9734113;	PubMed=9190810;	
RA	Loprasert S., Aitchatpongkul S., Whangsuk W., Mongkolksak S.,		
RT	"Isolation and analysis of the Xanthomonas Alkyl hydroperoxide		
RT	oxidase gene and the peroxide sensor regulator genes ahpc and ahpf-		
RT	oxxr-orfX."		

RL J. Bacteriol. 179:3944-3949(1997).
 DR EMBL: U94336; AAC45425.1; -
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 SQ SEQUENCE 187 AA; 20462 MW; 844A58ABC4E6AC4 CRC64;

Query Match 59.7%; Score 589.5; DB 2; Length 187;
 Best Local Similarity 56.9%; Pred. No. 8.1e-47;
 Matches 107; Conservative 33; Mismatches 47; Indels 1; Gaps 1;

QY 1 MSLNTRKPKKQAFKNGEIEITEKDTBGRMSVFFFPYADFTVCPTLGDVADHYE 60
 DB 1 MSLNTRKPKKQAFKNGEIEITEKDTBGRMSVFFFPYADFTVCPTLGDVADHYE 60
 QY 61 ELQKLGVDVAVSTDTHTFHKAHSSSETIAKIKYAMIGDPTGALTRFDMRDEGLAD 120
 DB 60 AFQKAGAEVYIVTDTDHSKVMHETSAVCKAOPPLIGDPTHLKTRAFGVHIEEGLAL 119
 QY 121 RATFVVDPGIIOAIEVTAEGISGDASDLRKIRAAQYVASHPEVCSPAKKEGEATLAP 180
 DB 120 RGTFLINEGVYIKLEIHDSIARDVETLTKLTAQGVANPNPGVCPAKKEGAKTLAP 179
 QY 181 SLDLVGKI 188
 DB 180 SLDLVGKI 187

RESULT 13
 ID 030738 PRELIMINARY; PRT; 187 AA.
 AC 030738;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ALKYL HYDROGEN PEROXIDE REDUCTASE.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JH2-7;
 RX MEDLINE=98117057; PubMed=9457879;
 RA Rice L.B., Caritas L.L.;
 RT "Transfer of Tn385, a composite, multiresistance chromosomal element
 from Enterococcus faecalis".
 RL J. Bacteriol. 180:714-721(1998).
 EMBL: AF016233; AAC46081.1; -
 HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 187 AA; 21090 MW; C400392C7CB98487 CRC64;

Query Match 57.1%; Score 563.5; DB 2; Length 187;
 Best Local Similarity 54.3%; Pred. No. 2.1e-44;
 Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSLNTRKPKKQAFKNGEIEITEKDTBGRMSVFFFPYADFTVCPTLGDVADHYE 60
 DB 1 MSLNTRKPKKQAFKNGEIEITEKDTBGRMSVFFFPYADFTVCPTLGDVADHYE 60
 QY 61 ELQKLGVDVAVSTDTHTFHKAHSSSETIAKIKYAMIGDPTGALTRFDMRDEGLAD 120
 DB 60 HLOELMCEVYVSDSHYHKKAMADATETIKTKYPMADPNQGLAKFVGVLDEASGMAY 119
 QY 121 RATFVVDPGIIOAIEVTAEGISGDASDLRKIRAAQYVASHPEVCSPAKKEGEATLAP 180
 DB 120 RASFIYSPGDIKSYEINDMIGIRNAEELVRKLEASQFAEHGDKVCPANMVGCEETIAP 179

QY 181 SLDLVGKI 188
 DB 180 SLDLVGKI 187

RESULT 14
 ID 083522 PRELIMINARY; PRT; 188 AA.
 AC 083522;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ALKYL HYDROPEROXIDE REDUCTASE (AHPc).
 GN TP0509.
 OS Treponema pallidum
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Winn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
 RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete".
 RL Science 281:375-388(1998).
 DR EMBL: AE001227; AAC65497.1; -
 DR HSSP: P30041; 1PRX.
 DR TIGR: TP0509;
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Complete proteome.
 SQ SEQUENCE 188 AA; 20709 MW; 44D2CFDPA3420AFE CRC64;

Query Match 49.5%; Score 488.5; DB 16; Length 188;
 Best Local Similarity 49.7%; Pred. No. 1.8e-37;
 Matches 93; Conservative 32; Mismatches 61; Indels 1; Gaps 1;

QY 2 SLNTRKPKKQAFKNGEIEITEKDTBGRMSVFFFPYADFTVCPTLGDVADHYE 61
 DB 3 SLGKRYIDPKLPAIVYGKFTVSNASIGSMAY-FEFPADFTVCPTLADLARVPS 61
 QY 62 LQKLGVDVAVSTDTHTFHKAHSSSETIAKIKYAMIGDPTGALTRFDMRDEGLAD 121
 DB 62 FVEIGCKVYVSTDSVYHKKAMADATDTIKNLPEMISDKAGLAFVGLVLPDTWHLAL 121
 QY 122 ATTFVVDPGIIOAIEVTAEGISGDASDLRKIRAAQYVASHPEVCSPAKKEGEATLAP 181
 DB 122 GTFVVDPEGLVKAFEVHDMGIGRDADELRLKYQSAQFAVAKHGQVCPARWKGAKTLKPG 181
 QY 182 SLDLVGKI 188
 DB 182 SLDLVGKI 188

RESULT 15
 ID 066779 PRELIMINARY; PRT; 211 AA.
 AC 066779;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ALKYL HYDROPEROXIDE REDUCTASE.
 GN AHPc1 OR AQ_486.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;

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